

<110> Genentech, Inc. Ashkenazi, Avi Botstein, David Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone Filvaroff, Ellen Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E. Goddard, A. Godowski, Paul J. Grimaldi, Christopher J. Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P. Pan, James Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Williams, P. Mickey Wood, William, I.

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Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr 100 105 110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys 120

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Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys 290 295 300

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24

<213> Homo sapiens

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<400> 23

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Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr

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<212> DNA

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28

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<212> PRT

<213> Homo sapiens

<400> 28

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Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr 35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly 50 55 60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe 65 70 75 80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr 85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg 100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala 115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser 130 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser 150 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val 170 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile 185 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly 215 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arq Asn 225 230 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg 250 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe 265 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp 305 315 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly 330 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Pro Gly Leu Pro Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro 375 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro 385 390 400 395 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

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Ala	Tyr 450	Lys	Leu	Thr	Trp	Val 455	Lys	Met	Gly	His	Ser 460	Leu	Val	Gly	Gly
Ile 465	Val	Gln	Glu	Arg	Ile 470	Val	Ser	Gly	Glu	Lys 475	Gln	His	Leu	Ser	Leu 480
Val	Asn	Leu	Glu	Pro 485	Arg	Ser	Thr	Tyr	Arg 490	Ile	Cys	Leu	Val	Pro 495	Leu
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His	Glu 530	Gln	Thr	Thr	Ser	His 535	Ser	Met	Gly	Ser	Pro 540	Phe	Leu	Leu	Ala
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Val	Phe	Cys	Trp	His 565	Met	His	Lys	Lys	Gly 570	Arg	Tyr	Thr	Ser	Gln 575	Lys
Trp	Lys	Tyr	Asn 580	Arg	Gly	Arg	Arg	Lys 585	Asp	Asp	Tyr	Cys	Glu 590	Ala	Gly
Thr	Lys	Lys 595	Asp	Asn	Ser	Ile	Leu 600	Glu	Met	Thr	Glu	Thr 605	Ser	Phe	Gln
Ile	Val 610	Ser	Leu	Asn	Asn	Asp 615	Gln	Leu	Leu	Lys	Gly 620	Asp	Phe	Arg	Leu
Gln 625	Pro	Ile	Tyr	Thr	Pro 630	Asn	Gly	Gly	Ile	Asn 635	Tyr	Thr	Asp	Cys	His 640
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<210> 31 <211> 22 <212> DNA <213> Artificial Sequence	
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<212> PRT

<213> Homo sapiens

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Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser 50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile 65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys 100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu 130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn 145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser 165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln 210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

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Asp	Gln	Thr 275	Thr	Cys	Arg	Ile	Gln 280	Asp	Leu	Cys	Ala	Met 285	Glu	Asp	His
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Val	Asp	Tyr	Cys	Ala 325	Ser	Glu	Asn	His	Gly 330	Cys	Glu	His	Glu	Cys 335	Val
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Lys	Pro 370	Gly	Cys	Glu	His	Glu 375	Cys	Val	Asn	Met	Glu 380	Glu	Ser	Tyr	Tyr
Cys 385	Arg	Cys	His	Arg	Gly 390	Tyr	Thr	Leu	Asp	Pro 395	Asn	Gly	Lys	Thr	Cys 400
Ser	Arg	Val	Asp	His 405	Cys	Ala	Gln	Gln	Asp 410	His	Gly	Cys	Glu	Gln 415	Leu
Cys	Leu	Asn	Thr 420	Glu	Asp	Ser	Phe	Val 425	Cys	Gln	Cys	Ser	Glu 430	Gly	Phe
Leu	Ile	Asn 435	Glu	Asp	Leu	Lys	Thr 440	Cys	Ser	Arg	Val	Asp 445	Tyr	Cys	Leu
Leu	Ser 450	Asp	His	Gly	Cys	Glu 455	Tyr	Ser	Cys	Val	Asn 460	Met	Asp	Arg	Ser
Phe 465	Ala	Cys	Gln	Cys	Pro 470	Glu	Gly	His	Val	Leu 475	Arg	Ser	Asp	Gly	Lys 480
Thr	Cys	Ala	Lys	Leu 485	Asp	Ser	Cys	Ala	Leu 490	Gly	Asp	His	Gly	Cys 495	Glu
His	Ser	Cys	Val	Ser	Ser	Glu	Asp	Ser 505	Phe	Val	Cys	Gln	Cys 510	Phe	Glu

- Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val 515 520 525
- Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp 530 540
- Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp 545 550 555
- Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly 565 570 575
- Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys 580 585 590
- Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys 595 600 605
- Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser 610 620
- Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile 625 630 635 640
- Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu 645 650 655
- Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn 660 670
- Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
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- Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu 725 730 735
- Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly 740 745 750
- Val Gly Lys Ala Ile Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro 755 760 765
- Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu 770 775 780
- Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser 785 790 795 800

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Gln	Pro	Thr	Glu 820	Ser	Glu	Pro	Val	Thr 825	Ile	Asn	Ile	Gln	Asp 830	Leu	Leu	
Ser	Cys	Ser 835	Asn	Phe	Ala	Val	Gln 840	His	Arg	Tyr	Leu	Phe 845	Glu	Glu	Asp	
Asn	Leu 850	Leu	Arg	Ser	Thr	Gln 855	Lys	Leu	Ser	His	Ser 860	Thr	Lys	Pro	Ser	
Gly 865	Ser	Pro	Leu	Glu	Glu 870	Lys	His	Asp	Gln	Cys 875	Lys	Cys	Glu	Asn	Leu 880	
Ile	Met	Phe	Gln	Asn 885	Leu	Ala	Asn	Glu	Glu 890	Val	Arg	Lys	Leu	Thr 895	Gln	
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Val	Leu 50	Pro	Ala	Trp	Tyr	Thr 55	Leu	His	Gly	Glu	Val 60	Ser	Ser	Ser	Gln
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Gly	Val	Ser	Leu 100	Val	Tyr	Ser	Met	Pro 105	Ser	Arg	Asn	Leu	Ser 110	Leu	Arg
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Ser	Phe	Gln 195	Thr	Phe	Phe	Ala	Pro 200	Ala	Leu	Asp	Val	Ile 205	Arg	Gly	Ser
Leu	Ser 210	Leu	Thr	Asn	Leu	Ser 215	Ser	Ser	Met	Ala	Gly 220	Val	Tyr	Val	Cys
Lys 225	Ala	His	Asn	Glu	Val 230	Gly	Thr	Ala	Gln	Cys 235	Asn	Val	Thr	Leu	Glu 240
Val	Ser	Thr	Gly	Pro 245	Gly	Ala	Ala	Val	Val 250	Ala	Gly	Ala	Val	Val 255	Gly
Thr	Leu	Val	Gly 260	Leu	Gly	Leu	Leu	Ala 265	Gly	Leu	Val	Leu	Leu 270	Tyr	His
Arg	Arg	Gly 275	Lys	Ala	Leu	Glu	Glu 280	Pro	Ala	Asn	Asp	Ile 285	Lys	Glu	Asp

Ala	Ile 290	Ala	Pro	Arg	Thr	Leu 295	Pro	Trp	Pro	Lys	Ser 300	Ser	Asp	Thr	Ile	
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Pro	Pro	His	Gly	Pro 325	Pro	Arg	Pro	Gly	Ala 330	Leu	Thr	Pro	Thr	Pro 335	Ser	
Leu	Ser	Ser	Gln 340	Ala	Leu	Pro	Ser	Pro 345	Arg	Leu	Pro	Thr	Thr 350	Asp	Gly	
Ala	His	Pro 355	Gln	Pro	Ile	Ser	Pro 360	Ile	Pro	Gly	Gly	Val 365	Ser	Ser	Ser	
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gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatggtg 180
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gcagtaacca agacaggttt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360
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Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn 50 55 60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly 65 70 75 80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln 85 90 95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn 100 105 110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys 115 120 125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln 130 135 140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile 145 150 155 160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys 165 170 175

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Val	Trp 210	Asp	Lys	Leu	Ser	Val 215	Asn	His	Arg	Arg	Thr 220	His	Leu	Thr	Lys
Leu 225	Met	His	Thr	Val	Glu 230	Gln	Ala	Thr	Leu	Arg 235	Ile	Ser	Gln	Ser	Phe 240
Gln	Lys	Thr	Thr	Glu 245	Phe	Asp	Thr	Asn	Ser 250	Thr	Asp	Ile	Ala	Leu 255	Lys
Val	Phe	Phe	Phe 260	Asp	Ser	Tyr	Asn	Met 265	Lys	His	Ile	His	Pro 270	His	Met
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Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu 610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln 660 665 670

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Leu Arg 690

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Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala

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			icia	l Sec	quen	ce										
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25

20

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- Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
- Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
- Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
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- Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
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- Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile 225 230 235 240
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- Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser 260 265 270
- Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn 275 280 285
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<sup>&</sup>lt;212> PRT

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Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro 50 55 60

- Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Gln Thr Asn Asn 65 70 75 80
- Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly 85 90 95
- Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
- Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu 115 120 125
- Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu 130 135 140
- Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe 145 150 155 160
- Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu 165 170 175
- Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile 180 185 190
- Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe 195 200 205
- Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu 210 215 220
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- Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile 260 265 270
- Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu 275 280 285
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- Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro 305 310 315 320
- Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu 325 330 335
- Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

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Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro 50 55 60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
65 70 75 80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser 85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala 100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val 115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn 130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met 145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val 165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala 180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val 195 200 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr 210 215 220

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- Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala 50 60
- Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
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- Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
- Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro 100 105 110
- Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser 115 120 125
- Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn 130 135 140
- Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp 145 150 155 160
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- Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser 180 185 190
- Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr 195 200 205
- Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His 210 215 220
- Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg 225 230 235 240
- Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr 245 250 255
- Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His 260 265 270
- Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr 275 280 285
- Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly 290 295 300

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Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser 355 360 365

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Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro 405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
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Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala 435 440 445

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Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu 485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu 500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr 515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr 530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala 545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu 565 570 575

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- Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn 50 55 60
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- Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser 210 215 220
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## oligonucleotide probe

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Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
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- Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro 260 265 270
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- Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala 290 295 300
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- Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala 325 330 335
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Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser 595 600 605

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- Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu 85 90 95
- Glu Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
  100 105 110
- Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu 115 120 125
- Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala 130 135 140
- Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met 145 150 155 160
- Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu 165 170 175
- Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr 180 185 190
- Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro 195 200 205
- Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val 210 215 220
- Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly 225 230 235 240
- Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys 245 250 255
- Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu 260 265 270
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- Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg 290 295 300
- Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro 305 310 315 320
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Ser Ser Al 385	a Thr Pro	Gln Ala Phe 390	Asp Ser Ser S	Ser Ala Val Va	1 Phe 400
Ile Phe Va	l Ser Thr 405	Ala Val Val	Val Leu Val : 410	Ile Leu Thr Me 41	
Val Leu Gl	y Leu Val 420	Lys Leu Cys	Phe His Glu 9	Ser Pro Ser Se 430	r Gln
Pro Arg Ly 43		Met Gly Pro 440	Pro Gly Leu (	Glu Ser Asp Pr 445	o Glu
Pro Ala Al 450	a Leu Gly	Ser Ser Ser 455		Thr Asn Asn Gl 160	y Val
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Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly 40

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr

55

45

- Val Pro Glu Gly Lys Val Val Leu Asn Phe Arg Phe Ile Asp Leu 65 70 75 80
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- His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro 100 105 110
- Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser 115 120 125
- Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala 130 135 140
- Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg 145 150 155 160
- Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro 165 170 175
- Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu 180 185 190
- Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
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- Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Glu Val Asn Asp Ala 210 215 220
- Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val 225 230 235 240
- Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu 245 250 255
- Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu 260 265 270
- Pro Thr Thr Glu Gln Pro Val Thr Thr Phe Pro Val Thr Thr 275 280 285
- Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr 290 295 300
- Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly 305 310 315 320
- Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val 325 330 335
- Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

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Asp Gly A	arg Gly	Lys Ile		Pro	Asn	Ser	Phe 395	Ile	Met	Met	Phe	Lys 400	
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<213> Homo sapiens

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Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu 65 70 75 80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly 85 90 95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser 100 105 110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro 115 120 125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro 130 135 140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu 145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly 165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Glu Ala Cys 180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His 195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro 210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His 225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys 245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg 260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg 275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu 290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln 305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr 325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala 340 345 350

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- Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu 50 55 60
- Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln 65 70 75 80
- Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr 85 90 95
- His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu 100 105 110
- Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala 115 120 125
- Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg 130 135 140
- Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr 145 150 155 160
- Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys 165 170 175
- Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg 180 185 190
- Pro Arg Gln Pro Leu Leu Gln Val Ser Val Gln Arg Glu His Leu 195 200 205
- Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln 210 215 220
- Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu 225 230 235 240
- Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro 245 250 255
- Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu 260 265 270
- Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe 275 280 285
- Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu 290 295 300
- Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu 305 310 315 320
- Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr 325 330 335

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Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
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<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
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<210> 116
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<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 116
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<210> 117
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<210> 118
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<212> DNA
<213> Homo sapiens
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aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120
ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180
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gaggaccggg tgaccttctt gccaactggt atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctcctctgcc 480
accattggga accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540
tacacctggt tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac ccgtgccttc 600
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tcaaatgctg tgcgcatgga agctgtggag cggaatgtgg gggtcatcgt ggcagccgtc 780
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tctagagcgg gaattagagg ctagagcggc tgaaatggtt gtttggtgat gacactgggg 1440
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<211> 299
<212> PRT
<213> Homo sapiens
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                  5
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             20
Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
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Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe 50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr 65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe 85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

<210> 121

<211> 50

<212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 121 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct	50
<210> 122 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 122 acacctggtt caaagatggg	20
<210> 123 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 123 taggaagagt tgctgaaggc acgg	24
<210> 124 <211> 20 <212> DNA <213> Artificial Sequence	
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<400> 124 ttgccttact caggtgctac	20
<210> 125 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	

## oligonucleotide probe

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<400> 125
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<210> 126
<211> 1210
<212> DNA
<213> Homo sapiens
<400> 126
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geetggagge egeeggage eegettteea eeeegacete tgeecaggee geaggeecca 180
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300
ggattgagec atgtacccag aaagggcaat geceaeegee eeetggeete eeetgeeeet 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
ggcgctgcga cggccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540
atgagatect eceggaaggg gatgecacaa ceatggggee eeetgtgaee etggagagtg 600
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtcccct 660
ctqtcqqqaa tgccacatcc tcctctqccq gagaccagtc tggaagccca actgcctatg 720
gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgccacc ctcctcttt 780
tgtcctggct ccgagcccag gagcgcctcc gcccactggg gttactggtg gccatgaagg 840
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aaqttqcttc
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<211> 282
<212> PRT
<213> Homo sapiens
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Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
                                                     30
             20
                                 25
Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
                             40
         35
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
                         55
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
                                         75
                     70
 65
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Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln 85 90 95

Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Leu Arg Asn Cys Ser 115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp 130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp 145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly 165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser 180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly 210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala 225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln 245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu 260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

24

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<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 129
                                                                   24
ttggttccac agccgagctc gtcg
<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 130
                                                                  50
gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc
<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens
<220>
<221> modified base
<222> (1837)
<223> a, t, c or g
<400> 131
cccacqcqtc cqqtctcqct cqctcqcqca qcqqcqqcaq caqaqqtcqc gcacagatgc 60
gggttagact ggcggggga ggaggcggag gagggaagga agctgcatgc atgagaccca 120
cagactettg caagetggat geeetetgtg gatgaaagat gtateatgga atgaaceega 180
qcaatqqaga tqqatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactettgge egtgateetg tggttteage tggegetgtg etteggeeet geacagetea 300
cgggcgggtt cgatgacctt caagtgtgtg ctgaccccgg cattcccgag aatggcttca 360
ggacccccag cggaggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg 540
aaqatgctga gattcataac aagacatata gacatggaga gaagctaatc atcacttgtc 600
atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcatta tgtcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
atcgctgctt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
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ctccaatggt gagtcacgga gatttcgtct gccacccgcg gccttgtgag cgctacaacc 960
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acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaatcag 1080
agcaaacqtq qcccaqcacc catqaqaccc tcctqaccac qtqqaagatt gtggcgttca 1140
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cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200 agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260 ttgtggtggt agacggcgtg cccgtcatgc tcccgtccta tgacgaagct gtgagtggcg 1320 gcttgagtgc cttaggcccc gggtacatgg cctctgtggg ccagggctgc cccttacccg 1380 tggacgacca gagccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440 agtcagaacc ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500 ctcccaggtg ccaagagac acccaccctg cttcggacaa ccctgacata attgccagca 1560 cggcagagag ggtggcatcc accagcccag gcatccatca tgcccactgg gtgttgttcc 1620 taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680 gttgatctt ggagttgatt cctttccttc tcttggttt agacaaatgt atcaagtcct 1800 gtttcttctt gaccagact gattaaaaa taaaagnaaa aaa 1843
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<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

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Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val 20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr 35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val 65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys 85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser 100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu 115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile 130 135 140

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile 165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

			180					185					190		
Ile	Ser	Glu 195	Leu	Gln	Thr	Ser	Phe 200	Pro	Val	Gly	Thr	Val 205	Ile	Ser	Tyr
Arg	Cys 210	Phe	Pro	Gly	Phe	Lys 215	Leu	Asp	Gly	Ser	Ala 220	Tyr	Leu	Glu	Cys
Leu 225	Gln	Asn	Leu	Ile	Trp 230	Ser	Ser	Ser	Pro	Pro 235	Arg	Cys	Leu	Ala	Leu 240
Glu	Ala	Gln	Val	Cys 245	Pro	Leu	Pro	Pro	Met 250	Val	Ser	His	Gly	Asp 255	Phe
Val	Cys	His	Pro 260	Arg	Pro	Cys	Glu	Arg 265	Tyr	Asn	His	Gly	Thr 270	Val	Val
Glu	Phe	Tyr 275	Cys	Asp	Pro	Gly	Tyr 280	Ser	Leu	Thr	Ser	Asp 285	Tyr	Lys	Tyr
Ile	Thr 290	Cys	Gln	Tyr	Gly	Glu 295	Trp	Phe	Pro	Ser	Tyr 300	Gln	Val	Tyr	Cys
Ile 305	Lys	Ser	Glu	Gln	Thr 310	Trp	Pro	Ser	Thr	His 315	Glu	Thr	Leu	Leu	Thr 320
Thr	Trp	Lys	Ile	Val 325	Ala	Phe	Thr	Ala	Thr 330	Ser	Val	Leu	Leu	Val 335	Leu
Leu	Leu	Val	Ile 340	Leu	Ala	Arg	Met	Phe 345	Gln	Thr	Lys ·	Phe	Lys 350	Ala	His
Phe	Pro	Pro 355	Arg	Gly	Pro	Pro	Arg 360	Ser	Ser	Ser	Ser	Asp 365	Pro	Asp	Phe
Val	Val 370	Val	Asp	Gly	Val	Pro 375	Val	Met	Leu	Pro	Ser 380	Tyr	Asp	Glu	Ala
Val 385	Ser	Gly	Gly	Leu	Ser 390	Ala	Leu	Gly	Pro	Gly 395	Tyr	Met	Ala	Ser	Val 400
Gly	Gln	Gly	Cys	Pro 405	Leu	Pro	Val	Asp	Asp 410	Gln	Ser	Pro	Pro	Ala 415	Tyr
Pro	Gly	Ser	Gly 420	Asp	Thr	Asp	Thr	Gly 425	Pro	Gly	Glu	Ser	Glu 430	Thr	Cys
Asp	Ser	Val 435	Ser	Gly	Ser	Ser	Glu 440	Leu	Leu	Gln	Ser	Leu 445	Tyr	Ser	Pro
Pro	Arg	Cys	Gln	Glu	Ser	Thr		Pro	Ala	Ser	Asp		Pro	Asp	Ile

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Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
465
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His Ala His Trp Val Leu Phe Leu Arg Asn
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<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 133
                                                                   23
atctcctatc gctgctttcc cgg
<210> 134
<211> 23
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 134
                                                                   23
agccaggatc gcagtaaaac tcc
<210> 135
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
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                                                                   50
<210> 136
<211> 1815
<212> DNA
<213> Homo sapiens
<400> 136
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gatgctgctg ccgcggttgc agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120
ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180
tacaqqccqt qctqctqqcc qtqctqctqq tqqqqctqcq ggccgcgacg ggtcgcctgc 240
tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300
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50

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agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480
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ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600
gcgaggtctg cgtggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagetge ettgaatetg geetacatee taateeceag catteceett etecteetee 900
ttgtggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960
cagaccetag cacaaaqaag caacacacca tetggeeete teeteaccag ggaaacagee 1020
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aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
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                                                                  1815
aqcaqqaaaa aaaaa
<210> 137
<211> 382
<212> PRT
<213> Homo sapiens
<400> 137
Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
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                  5
Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
             20
Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
                             40
Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
```

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser 65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn 85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Glu 100 105 110 Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr 115 120 125

Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser 130 135 140

Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro 145 150 155 160

Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys 165 170 175

Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala 180 185 190

Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro 195 200 205

Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys 210 215 220

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Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys 260 265 270

Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp 275 280 285

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Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly 305 310 315

Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val 325 330 335

Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly 340 345 350

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Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu 210 215 220

Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly 225 230 235 240

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Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val 325 330 335

Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp 340 345 350

Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu 355 360 365

Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val 370 375 380

Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn 385 390 395 400

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Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys 90

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr 110 105 100

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu 115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro 130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr 145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys 165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn 180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
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Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly 210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp 225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg 245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly 290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln 305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr 325 330 335

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## oligonucleotide probe

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Ala Tyr Leu Arg Asn Ala Val Val Ile Thr Gly Ala Thr Ser Gly
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Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu 50 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu 65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu 85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala 100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala 115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp 130 135

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys 145 150 155 160

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Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr 180 185 190

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Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala 180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile 195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly 210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu 225 230 235 240

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Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

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Lys \	Val	Trp	Lys 420	Ile	Phe	Lys	Ser	Asp 425	Ser	Glu	Val	Ala	Gly 430	Tyr	Ile	
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Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly 210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr 225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys 245 250 255

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Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg 325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe 340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr 355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser 370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr 385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala 405 410 415

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Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
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Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
                 85
Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
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385

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Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu

425

Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu

Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro

Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu

375

390

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440
445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp 450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val 465 470 475 480

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Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp 500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser 515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr 530 540

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Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln 595 600 605

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<213> Homo sapiens

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Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala 105 100 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp 120 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His 135 130 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly 170 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala 185 180 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu 200 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu 210 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro 235 230 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr 265 260 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly 280 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe 290 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly 310 315 305 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser 330 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

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Pro	Met	Thr	Phe	Glu 405	Ala	Val	Lys	Gln	Asp 410	His	Gly	Phe	Met	Leu 415	Туз
Arg	Thr	Tyr	Met 420	Thr	His	Thr	Ile	Phe 425	Glu	Pro	Thr	Pro	Phe 430	Trp	Va]
Pro	Asn	Asn 435	Gly	Val	His	Asp	Arg 440	Ala	Tyr	Val	Met	Val 445	Asp	Gly	Va]
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Lys	Ile	Asp 515	Asn	Leu	Val	Lys	Trp 520	Trp	Phe	Pro	Leu	Gln 525	Leu	Pro	Lys
Trp	Pro 530	Tyr	Pro	Gln	Ala	Pro 535	Ser	Gly	Pro	Thr	Phe 540	Tyr	Ser	Lys	Thi
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Trp	Thr	Lys	Gly	Gln 565	Val	Trp	Ile	Asn	Gly 570	Phe	Asn	Leu	Gly	Arg 575	Туі
Trp	Thr	Lys	Gln 580	Gly	Pro	Gln	Gln	Thr 585	Leu	Tyr	Val	Pro	Arg 590	Phe	Leı
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1947

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Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
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Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
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Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
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- Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu 210 215 220
- Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser 225 230 235 240
- Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu 245 250 255
- Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn 260 265 270
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- Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln 290 295 300
- Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile 305 310 315 320
- Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn 325 330 335
- Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu 340 345 350
- Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val 355 360 365
- Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile 370 375 380
- Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu 385 390 395 400
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- Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser 420 425 430
- Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu 435 440 445
- Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
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  455
  460
- Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

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<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

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<sup>&</sup>lt;211> 467

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Homo sapiens

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<210> 198

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Glu Th		Thr	Trp	Arg	Ser 375	Gln	Asn	Asp	Thr	Val 380	Thr	Pro	Asp	Val	
Trp Ty 385	r Thr	Ser	Lys	Pro 390	Lys	Glu	Lys	Leu	Val 395	Tyr	Ala	Ile	Phe	Leu 400	
Lys Tr	p Pro	Thr	Ser 405	Gly	Gln	Leu	Phe	Leu 410	Gly	His	Pro	Lys	Ala 415	Ile	
Leu Gl	ly Ala	Thr 420	Glu	Val	Lys	Leu	Leu 425	Gly	His	Gly	Gln	Pro 430	Leu	Asn	
Trp Il	le Ser 435		Glu	Gln	Asn	Gly 440	Ile	Met	Val	Glu	Leu 445	Pro	Gln	Leu	
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Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
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Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
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Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
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                        135
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<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

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Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys 130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val 145 150 155 160

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Pro	Gly	Val	Arg 340	Ser	Phe	Gly	Phe	Pro 345	Asp	Pro	Gln	Ser	Arg 350	Leu	Туз
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Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
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Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp 325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr 340 345 350

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Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala 420 425 430

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Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile 485 490 495

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Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met 165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp 180 185 190

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Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe 275 280 285

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<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

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Cys Thr Val Asp Ile Glu Ser Leu Thr Gly Tyr Arg Thr Tyr Arg
35 40 45

Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe
50 55 60

Tyr Ile Ser Leu Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr
65 70 75

Leu Trp Trp Met Leu Arg Arg Ser Leu Lys Lys Tyr Ser Phe Glu 80 85 90

Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

				95					100					105
Asn .	Asp	Phe	Ala	Phe 110	Met	Leu	His	Leu	Ile 115	Asp	Gln	Tyr	Asp	Pro 120
Leu	Tyr	Ser	Lys	Arg 125	Phe	Ala	Val	Phe	Leu 130	Ser	Glu	Val	Ser	Glu 135
Asn	Lys	Leu	Arg	Gln 140	Leu	Asn	Leu	Asn	Asn 145	Glu	Trp	Thr	Leu	Asp 150
Lys	Leu	Arg	Gln	Arg 155	Leu	Thr	Lys	Asn	Ala 160	Gln	Asp	Lys	Leu	Glu 165
Leu	His	Leu	Phe	Met 170	Leu	Ser	Gly	Ile	Pro 175	Asp	Thr	Val	Phe	Asp 180
Leu	Val	Glu	Leu	Glu 185	Val	Leu	Lys	Leu	Glu 190	Leu	Ile	Pro	Asp	Val 195
Thr	Ile	Pro	Pro	Ser 200	Ile	Ala	Gln	Leu	Thr 205	Gly	Leu	Lys	Glu	Leu 210
Trp	Leu	Tyr	His	Thr 215	Ala	Ala	Lys	Ile	Glu 220	Ala	Pro	Ala	Leu	Ala 225
Phe	Leu	Arg	Glu	Asn 230	Leu	Arg	Ala	Leu	His 235	Ile	Lys	Phe	Thr	Asp 240
Ile	Lys	Glu	Ile	Pro 245	Leu	Trp	Ile	Tyr	Ser 250	Leu	Lys	Thr	Leu	Glu 255
Glu	Leu	His	Leu	Thr 260	Gly	Asn	Leu	Ser	Ala 265	Glu	Asn	Asn	Arg	Tyr 270
Ile	Val	Ile	Asp	Gly 275	Leu	Arg	Glu	Leu	Lys 280	Arg	Leu	Lys	Val	Leu 285
Arg	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Leu	Pro	Gln	Val	Val	Thr	Asp
				290					295					300
Val	Gly	Val	His	Leu 305	Gln	Lys	Leu	Ser	Ile 310	Asn	Asn	Glu	Gly	Thr 315
Lys	Leu	Ile	Val	Leu 320	Asn	Ser	Leu	Lys	Lys 325	Met	Ala	Asn	Leu	Thr
Glu	Leu	Glu	Leu	Ile 335	Arg	Cys	Asp	Leu	Glu 340	Arg	Ile	Pro	His	Ser 345
Ile	Phe	Ser	Leu	His 350	Asn	Leu	Gln	Glu	Ile 355	Asp	Leu	Lys	Asp	Asn 360

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Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His
Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile
                                                          390
                 380
                                     385
Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu
                                     400
Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys
                                     415
Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe
                                     430
Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala
Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln
Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln
                                     475
Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile
                                     490
Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly
                 500
Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp
Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg
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                 530
Ala Asp Lys Glu Gln Ala
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<210> 252 <211> 24

<400> 251

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<400> 253
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<211> 1650
<212> DNA
<213> Homo Sapien
<400> 254
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 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150
 tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200
 ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcatgt 250
 ggcttcaggg cggtccaggc ggttctagca ctggatttgg aaactttgag 300
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350
 ccaggctgcc agtctcctat ttgtggataa tcccgtgggc actgggttca 400
 gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatggtggct 450
 tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500
 ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550
 cagctggcat tggtctagag ctttataagg ccattcagcg agggaccatc 600
 aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctcccctgt 650
 tgattcggtg ctctcctggg gaccttacct gtacagcatg tctcttctcg 700
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<sup>&</sup>lt;210> 255

<sup>&</sup>lt;211> 452

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Homo Sapien

<sup>&</sup>lt;400> 255

Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu
1 5 10 15

Leu Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp 20 25 30

Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val
35 40 45

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp 105 Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr 110 Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe 150 Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys 225 215 220 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr 270 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser 280 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His 300 290 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

<213> Homo Sapien

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				505					310					
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Gly	Gly	Gln	Ala	Thr 335	Asn	Val	Phe	Val	Asn 340	Met	Glu	Glu	Asp	Phe 345
Met	Lys	Pro	Val	Ile 350	Ser	Ile	Val	Asp	Glu 355	Leu	Leu	Glu	Ala	Gly 360
Ile	Asn	Val	Thr	Val 365	Tyr	Asn	Gly	Gln	Leu 370	Asp	Leu	Ile	Val	Asp 375
Thr	Met	Gly	Gln	Glu 380	Ala	Trp	Val	Arg	Lys 385	Leu	Lys	Trp	Pro	Glu 390
Leu	Pro	Lys	Phe	Ser 395	Gln	Leu	Lys	Trp	Lys 400	Ala	Leu	Tyr	Ser	Asp 405
Pro	Lys	Ser	Leu	Glu 410	Thr	Ser	Ala	Phe	Val 415	Lys	Ser	Tyr	Lys	Asn 420
Leu	Ala	Phe	Tyr	Trp 425	Ile	Leu	Lys	Ala	Gly 430	His	Met	Val	Pro	Ser 435
Asp	Gln	Gly	Asp	Met 440	Ala	Leu	Lys	Met	Met 445	Arg	Leu	Val	Thr	Gln 450
Gln	Glu													
<210>	> 256	5												
<211>	> 11(	00												
<212	> DNZ	A												

dos 256 ggccgcggga gaggaggcca tgggcgcgcg cggggcgctg ctgctggcgc 50 tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100 ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150 tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200 tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctgggca 250 ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300 cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350 gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

 cctcgctacc
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 accctatgac
 attgccttgg
 tgaagctgtc
 450

 tgcacctgtc
 acctacacta
 aacacatcca
 gcccatctgt
 ctccaggcct
 500

 ccacatttga
 gtttgagaac
 cggacagact
 gctgggtgac
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 550

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 tccaggaagt
 600

 tcaggtcgcc
 atcataaaca
 actctatgtg
 caaccacctc
 ttcctcaagt
 650

 acagtttccg
 caaggacatc
 tttggagaca
 tggtttgtg
 tggcaacgcc
 700

 caaggeggga
 aggatgcctg
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 tcaggtggac
 ccttggcctg
 750

 taacaagaat
 ggactgtggt
 atcagattgg
 agtcgtgagc
 tggggagtgg
 800

 gctgtgtgtcg
 gcccaatcgg
 cccggtgtct
 acaccaatat
 cagccaccac
 850

 tttgagtgga
 tccagaagct
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 cccagccag
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<400> 257

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Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser

20 25 30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly 35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
50 55 60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
65 70 75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu
80 85 90

<sup>&</sup>lt;210> 257

<sup>&</sup>lt;211> 314

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Homo Sapien

Ser	Asp	Pro	Ser	Gly 95	Trp	Met	Val	Gln	Phe 100	Gly	Gln	Leu	Thr	Ser 105
Met	Pro	Ser	Phe	Trp 110	Ser	Leu	Gln	Ala	Tyr 115	Tyr	Thr	Arg	Tyr	Phe 120
Val	Ser	Asn	Ile	Tyr 125	Leu	Ser	Pro	Arg	Tyr 130	Leu	Gly	Asn	Ser	Pro 135
Tyr	Asp	Ile	Ala	Leu 140	Val	Lys	Leu	Ser	Ala 145	Pro	Val	Thr	Tyr	Thr 150
Lys	His	Ile	Gln	Pro 155	Ile	Cys	Leu	Gln	Ala 160	Ser	Thr	Phe	Glu	Phe 165
Glu	Asn	Arg	Thr	Asp 170	Cys	Trp	Val	Thr	Gly 175	Trp	Gly	Tyr	Ile	Lys 180
Glu	Asp	Glu	Ala	Leu 185	Pro	Ser	Pro	His	Thr 190	Leu	Gln	Glu	Val	Gln 195
Val	Ala	Ile	Ile	Asn 200	Asn	Ser	Met	Cys	Asn 205	His	Leu	Phe	Leu	Lys 210
Tyr	Ser	Phe	Arg	Lys 215	Asp	Ile	Phe	Gly	Asp 220	Met	Val	Cys	Ala	Gly 225
Asn	Ala	Gln	Gly	Gly 230	Lys	Asp	Ala	Cys	Phe 235	Gly	Asp	Ser	Gly	Gly 240
Pro	Leu	Ala	Cys	Asn 245	Lys	Asn	Gly	Leu	Trp 250	Tyr	Gln	Ile	Gly	Val 255
Val	Ser	Trp	Gly	Val 260	Gly	Cys	Gly	Arg	Pro 265	Asn	Arg	Pro	Gly	Val 270
Tyr	Thr	Asn	Ile	Ser 275	His	His	Phe	Glu	Trp 280	Ile	Gln	Lys	Leu	Met 285
Ala	Gln	Ser	Gly	Met 290	Ser	Gln	Pro	Asp	Pro 295	Ser	Trp	Pro	Leu	Leu 300
Phe	Phe	Pro	Leu	Leu 305	Trp	Ala	Leu	Pro	Leu 310	Leu	Gly	Pro	Val	
-210.	25	٥												

<sup>&</sup>lt;210> 258

<sup>&</sup>lt;211> 2427

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo Sapien

<sup>&</sup>lt;400> 258

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cctcctaggg ctctttgccc tcatcctctc tggcaaatgc agttacagcc 100 cggagcccga ccagcggagg acgctgccc caggctgggt gtccctgggc 150 cqtqcqqacc ctqaqqaaga gctqaqtctc acctttqccc tqaqacagca 200 gaatgtggaa agactctcgg agctggtgca ggctgtgtcg gatcccagct 250 ctcctcaata cggaaaatac ctgaccctag agaatgtggc tgatctggtg 300 aggecatece cactgaceet ceacaeggtg caaaaatgge tettggcage 350 cggagcccag aagtgccatt ctgtgatcac acaggacttt ctgacttgct 400 ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagtttcat 450 cactatgtgg gaggacctac ggaaacccat gttgtaaggt ccccacatcc 500 ctaccagett ccacaggeet tggeceecca tgtggaettt gtggggggae 550 tgcaccgttt tcccccaaca tcatccctga ggcaacgtcc tgagccgcag 600 gtgacaggga ctgtaggcct gcatctgggg gtaaccccct ctgtgatccg 650 taagcgatac aacttgacct cacaagacgt gggctctggc accagcaata 700 acagccaagc ctgtgcccag ttcctggagc agtatttcca tgactcagac 750 ctggctcagt tcatgcgcct cttcggtggc aactttgcac atcaggcatc 800 ccagtctaga tgtgcagtac ctgatgagtg ctggtgccaa catctccacc 900 tgggtctaca gtagccctgg ccggcatgag ggacaggagc ccttcctgca 950 gtggctcatg ctgctcagta atgagtcagc cctgccacat gtgcatactg 1000 tgagctatgg agatgatgag gactccctca gcagcgccta catccagcgg 1050 gtcaacactg agctcatgaa ggctgccgct cggggtctca ccctgctctt 1100 cgcctcaggt gacagtgggg ccgggtgttg gtctgtctct ggaagacacc 1150 agttccgccc taccttccct gcctccagcc cctatgtcac cacagtggga 1200 ggcacatcct tccaggaacc tttcctcatc acaaatgaaa ttgttgacta 1250 tatcagtggt ggtggcttca gcaatgtgtt cccacggcct tcataccagg 1300 aggaagetgt aacgaagtte etgageteta gececeaeet gecaceatee 1350 agttacttca atgccagtgg ccgtgcctac ccagatgtgg ctgcactttc 1400

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Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

<sup>&</sup>lt;210> 259

<sup>&</sup>lt;211> 556

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Homo Sapien

<sup>&</sup>lt;400> 259

Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu 1 5 10 15

				20					25					30
Leu	Pro	Pro	Gly	Trp 35	Val	Ser	Leu	Gly	Arg 40	Ala	Asp	Pro	Glu	Glu 45
Glu	Leu	Ser	Leu	Thr 50	Phe	Ala	Leu	Arg	Gln 55	Gln	Asn	Val	Glu	Arg 60
Leu	Ser	Glu	Leu	Val 65	Gln	Ala	Val	Ser	Asp 70	Pro	Ser	Ser	Pro	Gln 75
Tyr	Gly	Lys	Tyr	Leu 80	Thr	Leu	Glu	Asn	Val 85	Ala	Asp	Leu	Val	Arg 90
Pro	Ser	Pro	Leu	Thr 95	Leu	His	Thr	Val	Gln 100	Lys	Trp	Leu	Leu	Ala 105
Ala	Gly	Ala	Gln	Lys 110	Cys	His	Ser	Val	Ile 115	Thr	Gln	Asp	Phe	Leu 120
Thr	Cys	Trp	Leu	Ser 125	Ile	Arg	Gln	Ala	Glu 130	Leu	Leu	Leu	Pro	Gly 135
Ala	Glu	Phe	His	His 140	Tyr	Val	Gly	Gly	Pro 145	Thr	Glu	Thr	His	Val 150
Val	Arg	Ser	Pro	His 155	Pro	Tyr	Gln	Leu	Pro 160	Gln	Ala	Leu	Ala	Pro 165
His	Val	Asp	Phe	Val 170	Gly	Gly	Leu	His	Arg 175	Phe	Pro	Pro	Thr	Ser 180
Ser	Leu	Arg	Gln	Arg 185	Pro	Glu	Pro	Gln	Val 190	Thr	Gly	Thr	Val	Gly 195
Leu	His	Leu	Gly	Val 200	Thr	Pro	Ser	Val	Ile 205	Arg	Lys	Arg	Tyr	Asn 210
Leu	Thr	Ser	Gln	Asp 215	Val	Gly	Ser	Gly	Thr 220	Ser	Asn	Asn	Ser	Gln 225
Ala	Cys	Ala	Gln	Phe 230	Leu	Glu	Gln	Tyr	Phe 235	His	Asp	Ser	Asp	Leu 240
Ala	Gln	Phe	Met	Arg 245	Leu	Phe	Gly	Gly	Asn 250	Phe	Ala	His	Gln	Ala 255
Ser	Val	Ala	Arg	Val 260	Val	Gly	Gln	Gln	Gly 265	Arg	Gly	Arg	Ala	Gly 270
Ile	Glu	Ala	Ser	Leu 275		Val	Gln	Tyr	Leu 280	Met	Ser	Ala	Gly	Ala 285

Asn	Ile	Ser	Thr	Trp 290	Val	Tyr	Ser	Ser	Pro 295	Gly	Arg	His	Glu	Gly. 300
Gln	Glu	Pro	Phe	Leu 305	Gln	Trp	Leu	Met	Leu 310	Leu	Ser	Asn	Glu	Ser 315
Ala	Leu	Pro	His	Val 320	His	Thr	Val	Ser	Tyr 325	Gly	Asp	Asp	Glu	Asp 330
Ser	Leu	Ser	Ser	Ala 335	Tyr	Ile	Gln	Arg	Val 340	Asn	Thr	Glu	Leu	Met 345
Lys	Ala	Ala	Ala	Arg 350	Gly	Leu	Thr	Leu	Leu 355	Phe	Ala	Ser	Gly	Asp 360
Ser	Gly	Ala	Gly	Cys 365	Trp	Ser	Val	Ser	Gly 370	Arg	His	Gln	Phe	Arg 375
Pro	Thr	Phe	Pro	Ala 380	Ser	Ser	Pro	Tyr	Val 385	Thr	Thr	Val	Gly	Gly 390
Thr	Ser	Phe	Gln	Glu 395	Pro	Phe	Leu	Ile	Thr 400	Asn	Glu	Ile	Val	Asp 405
Tyr	Ile	Ser	Gly	Gly 410	Gly	Phe	Ser	Asn	Val 415	Phe	Pro	Arg	Pro	Ser 420
Tyr	Gln	Glu	Glu	Ala 425	Val	Thr	Lys	Phe	Leu 430	Ser	Ser	Ser	Pro	His 435
Leu	Pro	Pro	Ser	Ser 440	Tyr	Phe	Asn	Ala	Ser 445	Gly	Arg	Ala	Tyr	Pro 450
Asp	Val	Ala	Ala	Leu 455	Ser	Asp	Gly	Tyr	Trp 460	Val	Val	Ser	Asn	Arg 465
Val	Pro	Ile	Pro	Trp 470	Val	Ser	Gly	Thr	Ser 475	Ala	Ser	Thr	Pro	Val 480
Phe	Gly	Gly	Ile	Leu 485	Ser	Leu	Ile	Asn	Glu 490	His	Arg	Ile	Leu	Ser 495
Gly	Arg	Pro	Pro	Leu 500	Gly	Phe	Leu	Asn	Pro 505	Arg	Leu	Tyr	Gln	Gln 510
His	Gly	Ala	Gly	Leu 515	Phe	Asp	Val	Thr	Arg 520	Gly	Cys	His	Glu	Ser 525
Cys	Leu	Asp	Glu	Glu 530	Val	Glu	Gly	Gln	Gly 535	Phe	Cys	Ser	Gly	Pro 540
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<211> 1638

<212> DNA

<213> Homo Sapien

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tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550
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Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr
35 40 45

Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu
50 55 60

Val Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu 65 70 75

Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu 80 85 90

Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile

95 100 105

Leu Ser Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser
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<sup>&</sup>lt;210> 261

<sup>&</sup>lt;211> 383

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Homo Sapien

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Arg	Phe	Ser	Ile	Phe 140	Gly	Lys	Asp	Phe	Leu 145	Leu	Asn	Tyr	Pro	Phe 150
Ser	Thr	Ser	Val	Lys 155	Leu	Ser	Thr	Gly	Cys 160	Thr	Gly	Thr	Leu	Val 165
Ala	Glu	Lys	His	Val 170	Leu	Thr	Ala	Ala	His 175	Cys	Ile	His	Asp	Gly 180
Lys	Thr	Tyr	Val	Lys 185	Gly	Thr	Gln	Lys	Leu 190	Arg	Val	Gly	Phe	Leu 195
Lys	Pro	Lys	Phe	Lys 200	Asp	Gly	Gly	Arg	Gly 205	Ala	Asn	Asp	Ser	Thr 210
Ser	Ala	Met	Pro	Glu 215	Gln	Met	Lys	Phe	Gln 220	Trp	Ile	Arg	Val	Lys 225
Arg	Thr	His	Val	Pro 230	Lys	Gly	Trp	Ile	Lys 235	Gly	Asn	Ala	Asn	Asp 240
Ile	Gly	Met	Asp	Tyr 245	Asp	Tyr	Ala	Leu	Leu 250	Glu	Leu	Lys	Lys	Pro 255
His	Lys	Arg	Lys	Phe 260	Met	Lys	Ile	Gly	Val 265	Ser	Pro	Pro	Ala	Lys 270
Gln	Leu	Pro	Gly	Gly 275	Arg	Ile	His	Phe	Ser 280	Gly	Tyr	Asp	Asn	Asp 285
Arg	Pro	Gly	Asn	Leu 290	Val	Tyr	Arg	Phe	Cys 295	Asp	Val	Lys	Asp	Gl·u 300
Thr	Tyr	Asp	Leu	Leu 305	Tyr	Gln	Gln	Суѕ	Asp 310	Ala	Gln	Pro	Gly	Ala 315
Ser	Gly	Ser	Gly	Val 320	Tyr	Val	Arg	Met	Trp 325	Lys	Arg	Gln	Gln	Gln 330
Lys	Trp	Glu	Arg	Lys 335	Ile	Ile	Gly	Ile	Phe 340	Ser	Gly	His	Gln	Trp 345
Val	Asp	Met	Asn	Gly 350	Ser	Pro	Gln	Asp	Phe 355	Asn	Val	Ala	Val	Arg 360
Ile	Thr	Pro	Leu	Lys 365	Tyr	Ala	Gln	Ile	Cys 370	Tyr	Trp	Ile	Lys	Gly 375
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<213> Homo Sapien

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<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

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175

180

170

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu 190 185 Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met 225 Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly 230 Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn 265 Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val 275 Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala 305 Arg Ser <210> 264 <211> 24 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 264 gtccgcaagg atgcctacat gttc 24 <210> 265 <211> 19 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 265 gcagaggtgt ctaaggttg 19 <210> 266 <211> 24

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<210> 278
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<400> 278
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<400> 279
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<400> 281
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<211> 61
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 atgctgtgtg ccggctact 119
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<211> 1875
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<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

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Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala 35 40 45

Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp
50 55 60

Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val 65 70 75

Trp Gly His Asn Lys Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe
80 85 90

Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu 95 100 105

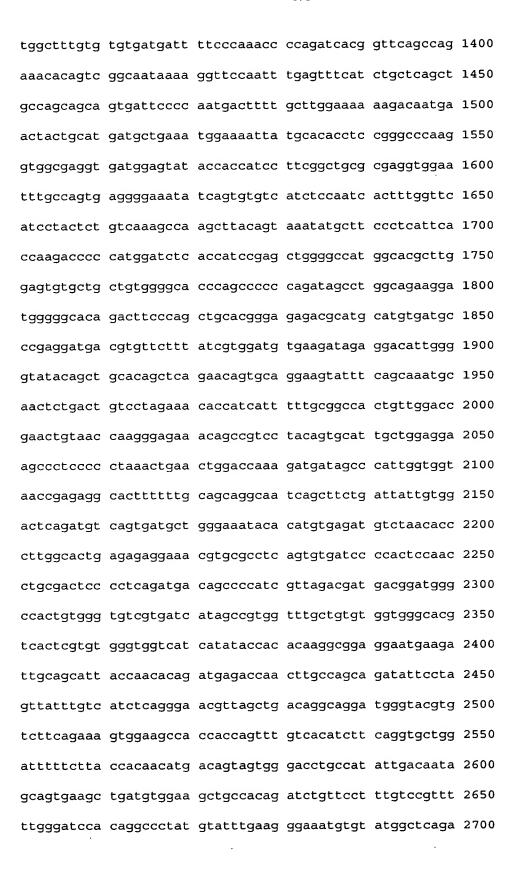
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110 115 120

Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala 125 130 135

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Gln	Gly	Val	Glu	Glu 155	Thr	Asn	Ile	Glu	Leu 160	Leu	Val	Cys	Asn	Tyr 165
Glu	Pro	Pro	Gly	Asn 170	Val	Lys	Gly	Lys	Arg 175	Pro	Tyr	Gln	Glu	Gly 180
Thr	Pro	Cys	Ser	Gln 185	Cys	Pro	Ser	Gly	Tyr 190	His	Cys	Lys	Asn	Ser 195
Leu	Cys	Glu	Pro	Ile 200	Gly	Ser	Pro	Glu	Asp 205	Ala	Gln	Asp	Leu	Pro 210
Tyr	Leu	Val	Thr	Glu 215	Ala	Pro	Ser	Phe	Arg 220	Ala	Thr	Glu	Ala	Ser 225
Asp	Ser	Arg	Lys	Met 230	Gly	Thr	Pro	Ser	Ser 235	Leu	Ala	Thr	Gly	Ile 240
Pro	Ala	Phẹ	Leu	Val 245	Thr	Glu	Val	Ser	Gly 250	Ser	Leu	Ala	Thr	Lys 255
Ala	Leu	Pro	Ala	Val 260	Glu	Thr	Gln	Ala	Pro 265	Thr	Ser	Leu	Ala	Thr 270
Lys	Asp	Pro	Pro	Ser 275	Met	Ala	Thr	Glu	Ala 280	Pro	Pro	Cys	Val	Thr 285
Thr	Glu	Val	Pro	Ser 290	Ile	Leu	Ala	Ala	His 295	Ser	Leu	Pro	Ser	Leu 300
Asp	Glu	Glu	Pro	Val 305	Thr	Phe	Pro	Lys	Ser 310	Thr	His	Val	Pro	Ile 315
Pro	Lys	Ser	Ala	Asp 320	Lys	Val	Thr	Asp	Lys 325	Thr	Lys	Val	Pro	Ser 330
Arg	Ser	Pro	Glu	Asn 335	Ser	Leu	Asp	Pro	Lys 340	Met	Ser	Leu	Thr	Gly 345
Ala	Arg	Glu	Leu	Leu 350	Pro	His	Ala	Gln	Glu 355	Glu	Ala	Glu	Ala	Glu 360
Ala	Glu	Leu	Pro	Pro 365	Ser	Ser	Glu	Val	Leu 370	Ala	Ser	Val	Phe	Pro 375
Ala	Gln	Asp	Lys	Pro 380	Gly	Glu	Leu	Gln	Ala 385	Thr	Leu	Asp	His	Thr 390
Gly	His	Thr	Ser	Ser 395	Lys	Ser	Leu	Pro	Asn 400	Phe	Pro	Asn	Thr	Ser 405

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 Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
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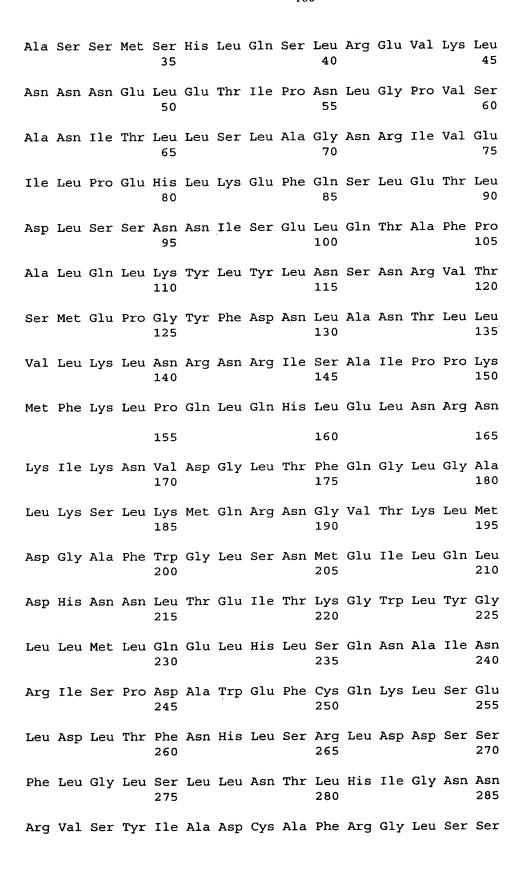
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Leu	His	Asp	Ala	Glu 485	Met	Glu	Asn	Tyr	Ala 490	His	Leu	Arg	Ala	Gln 495
Gly	Gly	Glu	Val	Met 500	Glu	Tyr	Thr	Thr	Ile 505	Leu	Arg	Leu	Arg	Glu 510
Val	Glu	Phe	Ala	Ser 515	Glu	Gly	Lys	Tyr	Gln 520	Cys	Val	Ile	Ser	Asn 525
His	Phe	Gly	Ser	Ser 530	Tyr	Ser	Val	Lys	Ala 535	Lys	Leu	Thr	Val	Asn 540
Met	Leu	Pro	Ser	Phe 545	Thr	Lys	Thr	Pro	Met 550	Asp	Leu	Thr	Ile	Arg 555

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Ala	Ala	Arg	Glu	Arg 590	Arg	Met	His	Val	Met 595	Pro	Glu	Asp	Asp	Val 600
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Cys	Thr	Ala	Gln	Asn 620	Ser	Ala	Gly	Ser	Ile 625	Ser	Ala	Asn	Ala	Thr 630
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Pro	Leu	Val	Val	Thr 680	Glu	Arg	His	Phe	Phe 685	Ala	Ala	Gly	Asn	Gln 690
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Ser	Tyr	Leu	Ser	Ser 800	Gln	Gly	Thr	Leu	Ala 805	Asp	Arg	Gln	Asp	Gly 810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser 820 815 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr 830 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr 855 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr 860 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr 895 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His 905 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp 930 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu 955 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn 965 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu 980 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg 1000 1005 995 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly 1015 1010 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn 1030 1025 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro 1050 1045 1040 Asn Phe Gln Ser Tyr Asp Leu Asp Thr

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50 55 60

Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
65 . 70 75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile 80 85 90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu 95 100 105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe 110 115 120

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg 125 130 135

Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu 140 145 150

Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser

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Ala	Asp	Leu	Asn	Val 365	Thr	Glu	Gly	Met	Ala 370	Ala	Glu	Leu	Lys	Cys 375
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<212> PRT

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Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
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Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
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Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu 80 85 90

Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met

95 100 105

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met 110 115 120

Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met 125 130 135

Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg 140 145 150

Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg 155 160 165

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Lys	Cys	His	Lys	Gly 200	Phe	Asp	Leu	Met	Tyr 205	Ile	Gly	Gly	Lys	Tyr 210
Gln	Cys	His	Asp	Ile 215	Asp	Glu	Cys	Ser	Leu 220	Gly	Gln	Tyr	Gln	Cys 225
Ser	Ser	Phe	Ala	Arg 230	Cys	Tyr	Asn	Val	Arg 235	Gly	Ser	Tyr	Lys	Cys 240
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Ile	Pro	Lys	Val	Met 260	Ile	Glu	Pro	Ser	Gly 265	Pro	Ile	His	Val	Pro 270
Lys	Gly	Asn	Gly	Thr 275	Ile	Leu	Lys	Gly	Asp 280	Thr	Gly	Asn	Asn	Asn 285
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Tyr	Ile	Pro	Pro	Ile 305	Ile	Thr	Asn	Arg	Pro 310	Thr	Ser	Lys	Pro	Thr 315
Thr	Arg	Pro	Thr	Pro 320	Lys	Pro	Thr	Pro	Ile 325	Pro	Thr	Pro	Pro	Pro 330
Pro	Pro	Pro	Leu	Pro 335	Thr	Glu	Leu	Arg	Thr 340	Pro	Leu	Pro	Pro	Thr 345
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His	Ser	Cys	Asn	Phe 395	Asp	His	Gly	Leu	Cys 400	Gly	Trp	Ile	Arg	Glu 405
Lys	Asp	Asn	Asp	Leu 410	His	Trp	Glu	Pro	Ile 415	Arg	Asp	Pro	Ala	Gly 420
Gly	Gln	Tyr	Leu		Val	Ser	Ala	Ala	Lys	Ala	Pro	Gly	Gly	Ļys

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Ala	Leu	Trp	Gly	Arg 485	Asn	Gly	Gly	His	Gly 490	Trp	Arg	Gln	Thr	Gln 495
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Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe 35 40 45

His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
50 55 60

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro 90 Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu 95 Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr 140 Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg 165 Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser 170 Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu 240 Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro 285 Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu 315 Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

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Arg	Pro	Glu	Thr	Glu 380	Tyr	Arg	Lys	Ala	Gln 385	Thr	Phe	Ser	Gly	His 390
Glu	Asp	Ala	Leu	Asp 395	Asp	Phe	Gly	Ile	Tyr 400	Glu	Phe	Val	Ala	Phe 405
Pro	Asp	Val	Ser	Gly 410	Val	Ser	Arg	Ile	Pro 415	Ser	Arg	Ser	Val	Pro 420
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Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln
50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
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Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys 110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile 125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser 140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys 155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser 170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu 185 190 195

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Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

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Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser 50 55 60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp
65 70 75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val 80 85 90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu 95 100 105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg 110 115 120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala 125 130 135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile 140 145 150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser 155 160 165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly
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Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln 185 190 195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu 200 205 210

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Glu	Arg	Ala	Gly	Gly 245	Asn	Leu	Arg	Tyr	Phe 250	Glu	Gln	Leu	Leu	Glu 255
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Ala	Thr	Pro	Glu	Gly 275	Ile	Tyr	Glu	Arg	Pro 280	Val	Asp	Tyr	Leu	Pro 285
Glu	Arg	Asp	Val	<b>T</b> yr 290	Glu	Ser	Leu	Cys	Arg 295	Gly	Glu	Gly	Val	Lys 300
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Asp	Glu	Trp	Asp	Ser 335	Pro	His	Ile	Val	Arg 340	Tyr	Tyr	Asp	Val	Met 345
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Asp	Asp	Pro	Val	Val 395	Ala	Arg	Val	Asn	Arg 400	Arg	Met	Gln	His	Ile 405
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Tyr	Gly	Val	Gly	Gly 425	Gln	Tyr	Glu	Pro	His 430	Phe	Asp	Phe	Ser	Arg 435
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Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
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Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
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Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg
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Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

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His	Gly	Asp	Glu	Arg 155	Pro	Ala	Trp	Leu	Met 160	Ser	Glu	Thr	Leu	Arg 165
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Pro	His	Leu	Asp	Gly 245	Cys	Arg	Gly	Asp	Ile 250	Leu	Ser	Ala	Arg	Pro 255
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Ser	Glu	Ile	Glu	Gln 335	Leu	Gln	Ala	Gln	Ile 340	Arg	Asn	Leu	Thr	Val 345
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Ala	Leu	Glu	Thr	Ala 410	Leu	Glu	Gln	Leu	Asn 415	Arg	Arg	Tyr	Gln	Pro 420
Arg	Leu	Arg	Phe	Gln 425	Lys	Gln	Arg	Leu	Leu 430	Asn	Gly	Tyr	Arg	Arg 435
Phe	Asp	Pro	Ala	Arg 440	Gly	Met	Glu	Tyr	Thr 445	Leu	Asp	Leu	Leu	Leu 450
Glu	Cys	Val	Thr	Gln 455	Arg	Gly	His	Arg	Arg 460	Ala	Leu	Ala		Arg 465
Val	Ser	Leu	Leu	Arg 470	Pro	Leu	Ser	Arg	Val 475	Glu	Ile	Leu	Pro	Met 480
Pro	Tyr	Val	Thr	Glu 485	Ala	Thr	Arg	Val	Gln 490	Leu	Val	Leu	Pro	Leu 495
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Ala	Ala	Asn	Val	Leu 515	Glu	Pro	Arg	Glu	His 520	Ala	Leu	Leu	Thr	Leu 525
Leu	Leu	Val	Tyr	Gly 530	Pro	Arg	Glu	Gly	Gly 535	Arg	Gly	Ala	Pro	Asp 540
Pro	Phe	Leu	Gly	Val 545	Lys	Ala	Ala	Ala	Ala 550	Glu	Leu	Glu	Arg	Arg 555
Tyr	Pro	Gly	Thr	Arg 560	Leu	Ala	Trp	Leu	Ala 565	Val	Arg	Ala	Glu	Ala 570
Pro	Ser	Gln	Val	Arg 575	Leu	Met	Asp	Val	Val 580	Ser	Lys	Lys	His	Pro 585
Val	Asp	Thr	Leu	Phe 590	Phe	Leu	Thr	Thr	Val 595	Trp	Thr	Arg	Pro	Gly 600
Pro	Glu	Val	Leu	Asn 605	Arg	Cys	Arg	Met	Asn 610	Ala	Ile	Ser	Gly	Trp 615
Gln	Ala	Phe	Phe	Pro 620	Val	His	Phe	Gln	Glu 625	Phe	Asn	Pro	Ala	Leu 630

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Lys	Val	Phe	Glu	Ser 110	Ile	Asn	Met	Asp	Thr 115	Asn	Asp	Met	Trp	Leu 120
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Gln	Tyr	Asn	Trp	Phe 140	Phe	Leu	Ala	Arg	Pro 145	Thr	Thr	Phe	Ala	Ile 150
Ile	Glu	Asn	Leu	Lys 155	Tyr	Phe	Leu	Leu	Lys 160	Lys	Asp	Pro	Ser	Gln 165
Pro	Phe	Tyr	Leu	Gly 170	His	Thr	Ile	Lys	Ser 175	Gly	Asp	Leu	Glu	Tyr 180
Val	Gly	Met	Glu	Gly 185	Gly	Ile	Val	Leu	Ser 190	Val	Glu	Ser	Met	Lys 195
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Cys	Leu	Lys	Tyr	Ala 230	Gly	Val	Phe	Ala	Glu 235	Asn	Ala	Glu	Asp	Ala 240
Asp	Gly	Lys	Asp	Val 245	Phe	Asn	Thr	Lys	Ser 250	Val	Gly	Leu	Ser	Ile 255
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<400> 352
ggattctaat acgactcact atagggcacc cacgcgtccg gctgctt 47
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<400> 353
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<210> 354
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
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<400> 354
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<223> Synthetic Oligonucleotide Probe
<400> 356
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<400> 357
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<400> 358
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<212> DNA
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 <400> 359
 ctatgaaatt aaccctcact aaagggacca aggccacaaa cggaaatc 48
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<210> 361
<211> 48
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<400> 361
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<210> 362
<211> 47
<212> DNA
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ggattctaat acgactcact atagggcccg cctcgctcct gctcctg 47
<210> 363
<211> 48
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<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 363
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<210> 364
<211> 47
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 364
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<223> Synthetic Oligonucleotide Probe
<400> 365
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<212> DNA
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<223> Synthetic Oligonucleotide Probe
<400> 366
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<210> 367
<211> 47
<212> DNA
<213> Artificial Sequence
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<400> 367
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<210> 368
<211> 47
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 368
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<210> 369
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<220>
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<210> 370
<211> 48
<212> DNA
<213> Artificial Sequence
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<400> 370
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<210> 371
<211> 48
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 371
ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48
<210> 372
<211> 47
<212> DNA
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<223> Synthetic Oligonucleotide Probe
<400> 372
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<210> 373
<211> 48
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe
<400> 373
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<210> 374
<211> 47
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
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<210> 375
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 375
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<210> 376
<211> 997
<212> DNA
<213> Homo Sapien
<400> 376
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 aaaaaatgaa ttcatctaaa tcatctgaaa cacaatgcac agagagagga 150
 tgcttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200
 atttctcaqt qcctqtttca tcaccagatg tgttgtgaca tttcgcatct 250
 ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300
 ctctcctqct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350
 gaactgggaa tattttcaat ccagctgcta cttcttttct actgacacca 400
 tttcctgggc gttaagttta aagaactgct cagccatggg ggctcacctg 450
 taaaatgaga gagtttttta ttggactgtc agaccaggtt gtcgagggtc 550
 agtggcaatg ggtggacggc acacctttga caaagtctct gagcttctgg 600
 gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650
 gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700
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<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

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Cys Phe Ser Ser Gln Met Phe Leu Trp Thr Val Ala Gly Ile Pro 20 25 30

Ile Leu Phe Leu Ser Ala Cys Phe Ile Thr Arg Cys Val Val Thr 35 40 45

Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro 50 55 60

Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser
65 70 75

Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser 80 85 90

Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu 95 100 105

Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser 110 115 120

Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg 125 130 135

Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp
140 145 150

Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp
155 160 165

Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala 170 175 180

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Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
                                      190
                 185
 Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile
 Asn Pro Leu Asn Lys Gly Lys Ser Leu
                 215
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<223> Synthetic Oligonucleotide Probe
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<211> 24
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<400> 379
tattcctacc atttcacaaa tccg 24
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ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg 49
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<211> 26
<212> DNA
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 gcagattttg aggacagcca cctcca 26
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<223> Synthetic oligonucleotide probe
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<400> 383
 cagactgagg gagatccgag a 21
<210> 384
<211> 20
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<400> 384
 cagctgccct tccccaacca 20
<210> 385
<211> 18
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 catcaagcgc ctctacca 18
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<210> 387
<211> 18
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<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe
<400> 387
gggccatcac agctccct 18
<210> 388
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 388
gggatgtggt gaacacagaa ca 22
<210> 389
<211> 22
<212> DNA
<213> Artificial Sequence
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<400> 389
tgccagctgc atgctgccag tt 22
<210> 390
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 390
cagaaggatg tcccgtggaa 20
<210> 391
<211> 17
<212> DNA
<213> Artificial Sequence
<220>
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gccgctgtcc actgcag 17
<210> 392
<211> 21
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<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 392
gacggcatcc tcagggccac a 21
<210> 393
<211> 20
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 393
 atgtcctcca tgcccacgcg 20
<210> 394
<211> 20
<212> DNA
<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe
<400> 394
gagtgcgaca tcgagagctt 20
<210> 395
<211> 18
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<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe
<400> 395
 ccgcagcctc agtgatga 18
<210> 396
<211> 21
<212> DNA
<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe
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gaagagcaca gctgcagatc c 21
<210> 397
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<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 397
 gaggtgtcct ggctttggta gt 22
<210> 398
<211> 20
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 398
cctctggcgc ccccactcaa 20
<210> 399
<211> 18
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<223> Synthetic oligonucleotide probe
<400> 399
 ccaggagagc tggcgatg 18
<210> 400
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<400> 400
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<210> 401
<211> 29
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<210> 402
<211> 22
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<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe
<400> 402
ggcagagact tccagtcact ga 22
<210> 403
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 403
 gccaagggtg gtgttagata gg 22
<210> 404
<211> 24
<212> DNA
<213> Artificial Sequence
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<400> 404
 caggcccct tgatctgtac ccca 24
<210> 405
<211> 23
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<213> Artificial Sequence
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<400> 405
 gggacgtgct tctacaagaa cag 23
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<210> 406
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
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<210> 407
<211> 31
<212> DNA
<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe
<400> 407
 tattcagagt tttccattgg cagtgccagt t 31
<210> 408
<211> 21
<212> DNA
<213> Artificial Sequence
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<400> 408
tctacatcag cctctctgcg c 21
<210> 409
<211> 23
<212> DNA
<213> Artificial Sequence
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<400> 409
 cgatcttctc cacccaggag cgg 23
<210> 410
<211> 18
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 410
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gccaggcctc acattcgt 18
<210> 411
<211> 23
<212> DNA
<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe
<400> 411
ctccctgaat ggcagcctga gca 23
<210> 412
<211> 24
<212> DNA
<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe
<400> 412
aggtgtttat taagggccta cgct 24
<210> 413
<211> 19
<212> DNA
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<223> Synthetic oligonucleotide probe
<400> 413
cagagcagag ggtgccttg 19
<210> 414
<211> 21
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 414
tggcggagtc ccctcttggc t 21
<210> 415
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
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<210> 416
<211> 21
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<223> Synthetic oligonucleotide probe
<400> 416
tcaaccctg accctttcct a 21
<210> 417
<211> 24
<212> DNA
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<223> Synthetic oligonucleotide probe
<400> 417
ggcaggggac aagccatete teet 24
<210> 418
<211> 20
<212> DNA
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<400> 418
gggactgaac tgccagcttc 20
<210> 419
<211> 22
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gggccctaac ctcattacct tt 22
<210> 420
<211> 23
<212> DNA
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<223> Synthetic oligonucleotide probe
<400> 420
tgtctgcctc agccccagga agg 23
<210> 421
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<400> 421
tctgtccacc atcttgcctt g 21
<210> 422
<211> 3554
<212> DNA
<213> Homo Sapien
<400> 422
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 cttcttcctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150
 tcaaatccag caatcgaacc ccagtggtac aggaatttga aagtgtggaa 200
 ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagtg 250
 gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300
 ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacâtccctg 350
 aagatetgga atgtgacacg gagagactea geeetttate getgtgaggt 400
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 ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500
 ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550
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 acaggcactt tggtgttcac tgctgttcac aaggacgact ctgggcagta 700
 ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750
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<210> 423

<211> 310

<212> PRT

<213> Homo Sapien

<400> 423

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Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
50 55 60

Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr 65 70 75

Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly 80 85 90

Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val 95 100 105

Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg 110 115 120

Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val 125 130 135

Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val

Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
155 160 165

His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu 170 175 180

Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe 185 190 195

His	Leu	Asn	Ser	Glu 200	Thr	Gly	Thr	Leu	Val 205	Phe	Thr	Ala	Val	His 210
Lys	Asp	Asp	Ser	Gly 215	Gln	Tyr	Tyr	Cys	Ile 220	Ala	Ser	Asn	Asp	Ala 225
Gly	Ser	Ala	Arg	Cys 230	Glu	Glu	Gln	Glu	Met 235	Glu	Val	Tyr	Asp	Leu 240
Asn	Ile	Gly	_	Ile 245	Ile	Gly	Gly	Val	Leu 250	Val	Val	Leu	Ala	Val 255
Leù	Ala	Leu	Ile	Thr 260	Leu	Gly	Ile	Cys	Cys 265	Ala	Tyr	Arg	Arg	Gly 270
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
				275					280					285
Gly	Lys	Pro	Asp	Gly 290	Val	Asn	Tyr	Ile	Arg 295	Thr	Asp	Glu	Glu	Gly 300
Asp	Phe	Arg	His	Lys 305	Ser	Ser		Val	Ile 310					